Listing of Claims:

1. (Original): A method of identifying at least one gene that is consistently expressed across different cell or tissue types in an organism, comprising:
(a) preparing gene expression profiles for different cell or tissue types from the organism;
(b) calculating the percent variability of expression using a one-factor or two-factor ANOVA analysis for at least one gene in each of the profiles across the different cell or tissue types; and
(c) selecting any gene whose percent variability of expression indicates that the gene is consistently expressed across the different cell or tissue types.

2. (Original): A method of claim 1, wherein the R^2 value from the one-factor or two-factor ANOVA analysis is a measure of percent variability of expression for the at least one gene.

3. (Original): A method of claim 2, wherein the R^2 value from the one-factor or two-factor ANOVA analysis is less than or equal to about 12.

4. (Original): A method of claim 1, wherein the different cell or tissue types comprise greater than about 10 different cell or tissue types.

5. (Original): A method of claim 1, wherein the different cell or tissue types comprise greater than about 25 different cell or tissue types.

6. (Original): A method of claim 1, wherein the different cell or tissue types comprise greater than about 50 different cell or tissue types.

7. (Original): A method of claim 4, wherein the cell or tissue types comprise normal and diseased cell or tissue types.

8. (Original): A method of claim 1, wherein the organism is a mammal.

9. (Original): A method of claim 8, wherein the mammal is a rat.

10. (Original): A method of claim 1, wherein the expression profiles are generated by querying a gene expression database for the expression level of at least one gene in different cell or tissue types from the organism or from a cell line.

11. (Original): A set of probes comprising at least two probes that specifically hybridize to a gene identified by the method of claim 1.

12. (Original): A set of probes according to claim 11, wherein the set comprises probes that specifically hybridize to at least about 10 genes.

13. (Original): A set of probes according to claim 11, wherein the set comprises probes that specifically hybridize to at least about 25 genes.

14. (Original): A set of probes according to claim 11, wherein the set comprises probes that specifically hybridize to at least about 50 genes.

15. (Original): A set of probes according to claim 11, wherein the set comprises probes that specifically hybridize to at least about 100 genes.

16. (Original): A set of probes according to claim 11, wherein the probes are attached to a single solid substrate.

17. (Original): A set of probes of claim 16, wherein the solid substrate is a chip.

18. (Original): A method of normalizing the data from a nucleic acid detection assay comprising:
(a) detecting the expression level for at least one gene in a nucleic acid sample; and
(b) normalizing the expression of said at least one gene with the detected expression of an control gene identified by the method of claim 1.

19. (Original): A method of claim 18, wherein step (b) comprises normalizing the expression level of said at least one gene with the expression levels of at least about 10 control genes.

20. (Original): A method of claim 18, wherein step (b) comprises normalizing the expression level of said at least one gene with the expression levels of at least about 25 control genes.

21. (Original): A method of claim 18, wherein step (b) comprises normalizing the expression level of said at least one gene with the expression levels of at least about 50 control genes.

22. (Original): A method of claim 18, wherein step (b) comprises normalizing the expression level of said at least one gene with the expression levels of at least about 100 control genes.

23. (Original): A method of claim 18, wherein the assay is quantitative.

24. (Original): A method of claim 18, wherein the assay is a hybridization reaction conducted on a solid substrate.

25. (Original): A method of claim 24, wherein the solid substrate is an oligonucleotide array.

26. (Original): A method of claim 25, wherein the array comprises oligonucleotide probes that are complementary to the control genes.

27. (Original): A method of claim 18, wherein the assay is a polymerase chain reaction.

28. (Original): A set of probes comprising at least two probes that specifically hybridize to a gene of Table 1 or a gene exhibiting about 95% nucleotide sequence identity to a gene of Table 1.

29. (Original): A set of probes of claim 28, comprising probes that specifically hybridize to at least about 10 genes of Table 1.

30. (Original): A set of probes of claim 28, comprising probes that specifically hybridize to at least about 25 genes of Table 1.

31. (Original): A set of probes of claim 28, comprising probes that specifically hybridize to at least about 50 genes of Table 1.

32. (Original): A set of probes of claim 28, comprising probes that specifically hybridize to at least about 100 genes of Table 1.

33. (Original): A set of probes of claim 28, wherein the probes are attached to a single solid substrate.

34. (Original): A set of probes of claim 33, wherein the solid substrate is a chip.

35. (Original): A method of normalizing the data from a nucleic acid detection assay comprising:
(a) detecting the expression level for at least one gene in a nucleic acid sample; and
(b) normalizing the expression of said at least one gene with the detected expression of a control gene of Table 1.

36. (Original): A method of claim 35, wherein step (b) comprises normalizing the expression level of said at least one gene with the expression levels of at least about 10 control genes of Table 1.

37. (Original): A method of claim 35, wherein step (b) comprises normalizing the expression level of said at least one gene with the expression levels of at least about 25 control genes of Table 1.

38. (Original): A method of claim 35, wherein step (b) comprises normalizing the expression level of said at least one gene with the expression levels of at least about 50 control genes of Table 1.

39. (Original): A method of claim 35, wherein step (b) comprises normalizing the expression level of said at least one gene with the expression levels of at least about 100 control genes of Table 1.

40. (Original): A method of claim 35, wherein the assay is quantitative.

41. (Original): A method of claim 35, wherein the assay is a hybridization reaction conducted on a solid substrate.

42. (Original): A method of claim 41, wherein the solid substrate is an oligonucleotide array.

43. (Original): A method of claim 42, wherein the array comprises oligonucleotide probes that are complementary to the control genes.

44. (Original): A method of claim 35, wherein the assay is a polymerase chain reaction.

45. (Original): A method of claim 18, wherein the normalizing of step (b) comprises dividing the expression level for said at least one gene by the detected expression level of said control gene.

46. (Original): A method of identifying at least one gene that is consistently expressed across different cell or tissue types in an organism or cell line, comprising:
(a) querying a gene expression database for the expression level of at least one gene in different cell or tissue types from the organism or cell lines;
(b) calculating the percent variability of expression using a one-factor or two-factor ANOVA analysis for said at least one gene across the different cell or tissue types or cell lines; and
(c) identifying at least one gene whose percent variability of expression indicates that the gene is consistently expressed across the different cell or tissue types or cell lines.

47. (Original): A method of claim 46, wherein the R^2 value from the one-factor or two-factor ANOVA analysis is a measure of percent variability of expression for the at least one gene.

48. (Original): A method of claim 47, wherein the R^2 value from the one-factor or two-factor ANOVA analysis is less than or equal to about 12.

49. (Original): A method of claim 46, wherein the different cell or tissue types comprise greater than about 10 different cell or tissue types.

50. (Original): A method of claim 46, wherein the different cell or tissue types comprise greater than about 25 different cell or tissue types.

51. (Original): A method of claim 46, wherein the different cell or tissue types comprise greater than about 50 different cell or tissue types.

52. (Original): A method of claim 46, wherein the cell or tissue types comprise normal and diseased cell or tissue types.

53. (Original): A method of claim 46, wherein the organism is a mammal.

54. (Original): A method of claim 54, wherein the mammal is a rat.

55. (Original): A method of identifying a nucleic acid molecule whose level of expression is invariant across two or more cell or tissue samples, comprising:
(a) determining the variation in the expression level of the nucleic acid molecule (R^2 value) from two or more cell or tissue samples by one factor or two factor analysis of variation (ANOVA);
(b) comparing the R^2 value for the nucleic acid molecule to a threshold value, wherein the expression level of the nucleic acid molecule is considered to be invariant if the R^2 value is less than the threshold value; and
(c) identifying a nucleic acid molecule whose level of expression is invariant across two or more cell or tissue samples.

56. (Original): A method of normalizing data from a nucleic acid detection assay comprising:
(a) detecting the expression level for at least one gene in a nucleic acid sample; and
(b) normalizing the expression level of said at least one gene with the detected expression level of an invariant gene identified by the method of claim 55.